

1632



1632

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,904A

DATE: 02/06/2002

TIME: 09:38:08

Input Set : A:\seqlist.asc.txt

Output Set: N:\CRF3\02062002\I721904A.raw

RECEIVED
FEB 14 2002
TECH CENTER 1600/2900
P.5

ENTERED

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3 <110> APPLICANT: JULIUS, Michael H.
4   FILIPP, Dominik
6 <120> TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
7   LAIT/sCD14-PROTEIN
9 <130> FILE REFERENCE: 47841/00063
11 <140> CURRENT APPLICATION NUMBER: US 09/721,904A
12 <141> CURRENT FILING DATE: 2000-11-27
14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00482
15 <151> PRIOR FILING DATE: 1999-05-27
17 <150> PRIOR APPLICATION NUMBER: US 60/086,884
18 <151> PRIOR FILING DATE: 1998-05-27
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: Wordperfect 9.0
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25 <211> LENGTH: 1122
26 <212> TYPE: DNA
27 <213> ORGANISM: bovine
29 <400> SEQUENCE: 1
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34 gatccgaagc ctgactggct tagcgccgtt cagtgtatgg ttgccgtcga ggtggagatc      180
36 agtgccggcg gccgcagcct ggaacagttt ctcaaggagg ccgacaccaa cccgaagcag      240
38 tatgctgaca caatcaaggc tctgcgcgtt cggcgactca agctggggcg tgcacagggt      300
40 cctgctcagc ttctggctgc cgttctgcgc gcgctcgggt actctcgtct caaggaactg      360
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44 cctgcgctca ccaccctcag tctgcgtaac gtatcgtgga caacaggagg tgcctggctc      480
46 ggcgaactgc agcagtggct caagcctggg ctgagggtgc tgaacattgc ccaagcacac      540
48 tcgcttgccct ttccgtgcgc agggctctcc accttcgagg cgctcaccac cctagacctg      600
50 tctgacaatc ccagtctcgg cgacacgggg ctgatggcag ctctctgtcc gaacaagttc      660
52 ccggccctcc aatatctagc gctacgcaac gcggggatgg agacgccgag cggcgtgtgc      720
54 gcggcgctgg cggcagcgag ggtgcagccc caaagcctgg acctcagcca caactcgtctg      780
56 cgcgtcaccg ccccggtgct taccgatgt gtctggccca gtgcactaag gtctctcaat      840
58 ttgtcgttcg ctgggctgga gcaagtgcct aagggaactgc ccctaagct cagcgtgctt      900
60 gatctcagct gcaacaagct aagcaggagg ccgcggcgag acgagctgcc cgaggtaaat      960
62 gacctgactc tggacggaaa tccctttctg gaccctggag ccctccagca ccaaaatgac      1020
64 ccgatgatct ccggcggtgt cccagcctgt gcgcgttctg ccttgaccat ggggggtgtca      1080
66 ggagccctgg cgctgcttca aggagccga ggcttcgcgt aa      1122
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70 <211> LENGTH: 1128
71 <212> TYPE: DNA
72 <213> ORGANISM: human
74 <400> SEQUENCE: 2
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77 acgccagaac cttgtgagct ggacgatgaa gatttccgct gcgtctgcaa cttctccgaa      120
79 cctcagcccg actggtccga agccttccag tgtgtgtctg cagtagaggt ggagatccat      180
81 gccggcggtc tcaacctaga gccgtttcta aagcgctcg atgcggacgc cgaccgcgg      240
83 cagtatgctg acacggtcaa ggctctccgc gtgcggcggc tcacagtggg agccgcacag      300
85 gttcctgctc agctactggt aggcgcctg cgtgtgctag cgtactccc cctcaaggaa      360
87 ctgacgctcg aggacctaaa gataaccgct accatgcctc cgctgcctct ggaagccaca      420
89 ggacttgcac tttccagctt gcgcctacgc aacgtgtcgt gggcgacagg gcgttcttgg      480
91 ctgcgccgagc tgcagcagtg gctcaagcca ggctcaagg tactgagcat tgcccaagca      540
93 cactgccttg ccttttcttg cgaacagggt cgcgcttcc cgcccttac cagcctagac      600
95 ctgtctgaca atcctggact gggcgaacgc ggactgatgg cggctctctg tccccacaag      660
97 tccccggcca tccagaatct agcgctgcgc aacacaggaa tggagacgcc cacaggcgtg      720
99 tgcgcgcac tggcggcggc aggtgtgcag cccacagcc tagacctcag ccacaactcg      780
101 ctgcgcgcca ccgtaaacc tagcgtccg agatgcatgt ggtccagcgc cctgaactcc      840
103 ctcaatctgt cgttcgctgg gctggaacag gtgcctaaag gactgccagc caagctcaga      900
105 gtgctcgatc tcagctgcaa cagactgaac agggcgccgc agcctgacga gctgcccag      960
107 gtggataacc tgacactgga cgggaatccc ttctgtgtcc ctggaactgc cctccccac      1020
109 gagggctcaa tgaactccgg cgtggtccca gcctgtgcac gttcgacct gtcggtggg      1080
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115 <211> LENGTH: 1101
116 <212> TYPE: DNA
117 <213> ORGANISM: murine
119 <400> SEQUENCE: 3
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124 tggtcacag ctttcaattg tttgggggcy gcagatgtgg aattgtacgg cggcgccgc      180
126 agcctggaat accttctaaa gcgtgtggac acggaagcag atctggggca gttactgat      240
128 attatcaagt ctctgtcctt aaagcggctt acggtgcggg ccgcgcggat tcctagtcgg      300
130 attctattcg gagccctgcg tgtgtctcgg atttccggcc tccaggaaact gactcttgaa      360
132 aatctcgagg taaccggcac cgcgccgcca ccgcttctgg aagccaccgg acccgatctc      420
134 aacatcttga acctccgcaa cgtgtcgtgg gcaacaagg atgcctggct cgcagaactg      480
136 cagcagtggc taaagcctgg actcaaggta ctgagtattg cccaagcaca ctactcaac      540
138 ttttctgcy aacaggctcg cgtcttccct gccctctcca ccttagacct gtctgacaat      600
140 cctgaattgg gcgagagagg actgatctca gccctctgtc ccctcaagtt cccgaccctc      660
142 caagttttag cgctgcgtaa cgcggggatg gagacgcca gcgcggtgtg ctctgcgctg      720
144 gccgcagcaa ggttacagct gcaaggacta gaccttagtc acaattcact gcgggatgct      780
146 gcaggcgctc cgagttgtga ctggcccagt cagctaaact cgctcaatct gtctttcact      840
148 gggctgaagc aggtacctaa agggctgcca gccaagetca gcgtgctgga tctcagttac      900
150 aacaggctgg ataggaaccc tagcccagat gagctgcccc aagtggggaa cctgtcactt      960
152 aaaggaaatc cttttttgga ctctgaatcc cactcggaga agtttaactc tggcgtagtc      1020
154 accgccggag ctccatcatc ccaagcagtg gccttgtcag gaactctggc tttgtccta      1080
156 ggagatcgcc tctttgttta a
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 373
161 <212> TYPE: PRT
162 <213> ORGANISM: bovine
164 <400> SEQUENCE: 4
165 Met Val Cys Val Pro Tyr Leu Leu Leu Leu Leu Leu Pro Ser Leu Leu
166 1 5 10 15

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168 Arg Val Ser Ala Asp Thr Thr Glu Pro Cys Glu Leu Asp Asp Asp Asp
169                20                25                30
171 Phe Arg Cys Val Cys Asn Phe Thr Asp Pro Lys Pro Asp Trp Ser Ser
172                35                40                45
174 Ala Val Gln Cys Met Val Ala Val Glu Val Glu Ile Ser Ala Gly Gly
175                50                55                60
177 Arg Ser Leu Glu Gln Phe Leu Lys Gly Ala Asp Thr Asn Pro Lys Gln
178 65                70                75                80
180 Tyr Ala Asp Thr Ile Lys Ala Leu Arg Val Arg Arg Leu Lys Leu Gly
181                85                90                95
183 Ala Ala Gln Val Pro Ala Gln Leu Leu Val Ala Val Leu Arg Ala Leu
184                100                105                110
186 Gly Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Glu Val Thr
187                115                120                125
189 Gly Pro Thr Pro Pro Thr Pro Leu Glu Ala Ala Gly Pro Ala Leu Thr
190                130                135                140
192 Thr Leu Ser Leu Arg Asn Val Ser Trp Thr Thr Gly Gly Ala Trp Leu
193 145                150                155                160
195 Gly Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Arg Val Leu Asn Ile
196                165                170                175
198 Ala Gln Ala His Ser Leu Ala Phe Pro Cys Ala Gly Leu Ser Thr Phe
199                180                185                190
201 Glu Ala Leu Thr Thr Leu Asp Leu Ser Asp Asn Pro Ser Leu Gly Asp
202                195                200                205
204 Thr Gly Leu Met Ala Ala Leu Cys Pro Asn Lys Phe Pro Ala Leu Gln
205                210                215                220
207 Tyr Leu Ala Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys
208 225                230                235                240
210 Ala Ala Leu Ala Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser
211                245                250                255
213 His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp
214                260                265                270
216 Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln
217                275                280                285
219 Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys
220                290                295                300
222 Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn
223 305                310                315                320
225 Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln
226                325                330                335
228 His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg
229                340                345                350
231 Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly
232                355                360                365
234 Ala Arg Gly Phe Ala
235                370
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 375
240 <212> TYPE: PRT

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241 <213> ORGANISM: human
243 <400> SEQUENCE: 5
244 Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Pro Leu Val His
245 1 5 10 15
247 Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe
248 20 25 30
250 Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala
251 35 40 45
253 Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu
254 50 55 60
256 Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg
257 65 70 75 80
259 Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val
260 85 90 95
262 Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
263 100 105 110
265 Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile
266 115 120 125
268 Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu
269 130 135 140
271 Ser Ser Leu Arg Leu Arg Asn Val Ser Trp Ala Thr Gly Arg Ser Trp
272 145 150 155 160
274 Leu Ala Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser
275 165 170 175
277 Ile Ala Gln Ala His Ser Pro Ala Phe Ser Tyr Glu Gln Val Arg Ala
278 180 185 190
280 Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly
281 195 200 205
283 Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile
284 210 215 220
286 Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val
287 225 230 235 240
289 Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu
290 245 250 255
292 Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys
293 260 265 270
295 Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu
296 275 280 285
298 Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu
299 290 295 300
301 Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu
302 305 310 315 320
304 Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr
305 325 330 335
307 Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys
308 340 345 350
310 Ala Arg Ser Thr Leu Ser Val Gly Val Ser Gly Thr Leu Val Leu Leu
311 355 360 365
313 Gln Gly Ala Arg Gly Phe Ala

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314      370      375
317 <210> SEQ ID NO: 6
318 <211> LENGTH: 366
319 <212> TYPE: PRT
320 <213> ORGANISM: murine
322 <400> SEQUENCE: 6
323 Met Glu Arg Val Leu Gly Leu Leu Leu Leu Leu Val His Ala Ser
324 1      5      10      15
326 Pro Ala Pro Pro Glu Pro Cys Glu Leu Asp Glu Glu Ser Cys Ser Cys
327      20      25      30
329 Asn Phe Ser Asp Pro Lys Pro Asp Trp Ser Ser Ala Phe Asn Cys Leu
330      35      40      45
332 Gly Ala Ala Asp Val Glu Leu Tyr Gly Gly Gly Arg Ser Leu Glu Tyr
333      50      55      60
335 Leu Leu Lys Arg Val Asp Thr Glu Ala Asp Leu Gly Gln Phe Thr Asp
336 65      70      75      80
338 Ile Ile Lys Ser Leu Ser Leu Lys Arg Leu Thr Val Arg Ala Ala Arg
339      85      90      95
341 Ile Pro Ser Arg Ile Leu Phe Gly Ala Leu Arg Val Leu Gly Ile Ser
342      100     105     110
344 Gly Leu Gln Glu Leu Thr Leu Glu Asn Leu Glu Val Thr Gly Thr Ala
345      115     120     125
347 Pro Pro Pro Leu Leu Glu Ala Thr Gly Pro Asp Leu Asn Ile Leu Asn
348      130     135     140
350 Leu Arg Asn Val Ser Trp Ala Thr Arg Asp Ala Trp Leu Ala Glu Leu
351 145     150     155     160
353 Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser Ile Ala Gln Ala
354      165     170     175
356 His Ser Leu Asn Phe Ser Cys Glu Gln Val Arg Val Phe Pro Ala Leu
357      180     185     190
359 Ser Thr Leu Asp Leu Ser Asp Asn Pro Glu Leu Gly Glu Arg Gly Leu
360      195     200     205
362 Ile Ser Ala Leu Cys Pro Leu Lys Phe Pro Thr Leu Gln Val Leu Ala
363      210     215     220
365 Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys Ser Ala Leu
366 225     230     235     240
368 Ala Ala Ala Arg Val Gln Leu Gln Gly Leu Asp Leu Ser His Asn Ser
369      245     250     255
371 Leu Arg Asp Ala Ala Gly Ala Pro Ser Cys Asp Trp Pro Ser Gln Leu
372      260     265     270
374 Asn Ser Leu Asn Leu Ser Phe Thr Gly Leu Lys Gln Val Pro Lys Gly
375      275     280     285
377 Leu Pro Ala Lys Leu Ser Val Leu Asp Leu Ser Tyr Asn Arg Leu Asp
378      290     295     300
380 Arg Asn Pro Ser Pro Asp Glu Leu Pro Gln Val Gly Asn Leu Ser Leu
381 305     310     315     320
383 Lys Gly Asn Pro Phe Leu Asp Ser Glu Ser His Ser Glu Lys Phe Asn
384      325     330     335
386 Ser Gly Val Val Thr Ala Gly Ala Pro Ser Ser Gln Ala Val Ala Leu

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/721,904A

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Input Set : A:\seqlist.asc.txt

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L:120 M:112 C: (48) String data converted to lower case,

M:112 Repeated in SeqNo=3

L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7